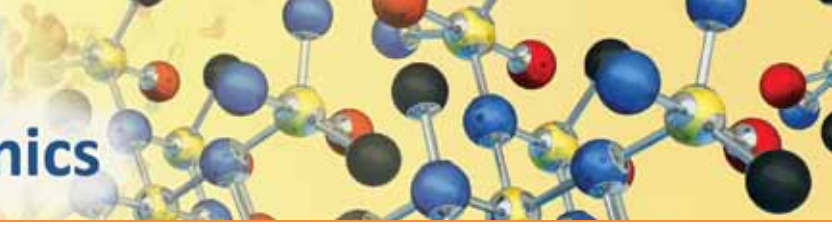
National Cancer Institute

Office of Cancer Genomics



MISSION

The National Cancer Institute's **Office of Cancer Genomics** (OCG) aims to advance the understanding of cancer at the molecular level with the ultimate goal of improving clinical outcomes. OCG's research programs conduct systematic characterization of tumor genomes and work rapidly towards translating the resulting molecular insights into improved cancer management and treatment strategies.

Learn about OCG and sign up for OCG mailing list:

http://ocg.cancer.gov

GOALS

- Guide, manage, and maintain major cancer genomics research programs
- Support research that translates the growing amount of genomics information into therapeutic strategies for individual patients (i.e. precision medicine)
- Provide easy access to data generated, technology, methods, informatics tools and material resources to program researchers and the research community at large

PROGRAMS

OCG supports large-scale cancer genomics research projects through highly-focused initiatives, or programs. The data generated by the projects are disseminated to the research community via program-specific data matrices. OCG initiatives promote advances in technology-based infrastructure and create valuable experimental reagents and tools. They also encourage collaboration by interconnections with other genomics and cancer projects in order to accelerate translation of findings into the clinic.

http://ocg.cancer.gov/programs

Therapeutically Applicable Research to Generate Effective Treatments (TARGET)

TARGET is a comprehensive molecular characterization initiative that utilizes state-of the-art genomics tools to identify molecular changes that drive the most prevalent childhood cancers: acute lymphoblastic leukemia, acute myeloid leukemia, neuroblastoma, osteosarcoma, and several types of kidney tumors. Emphasis is placed on finding alterations that can be targeted with therapeutic agents. TARGET is organized into a collaborative network of disease-specific project teams that leverage the strengths and resources of various NCI programs, including the Children's Oncology Group (COG), Cancer Therapy Evaluation Program (CTEP) and Office of Cancer Genomics, to fulfill its mission. This cooperative approach allows for efficient discovery and translation of scientific insights so that diagnostic and prognostic markers, along with more effective, less toxic treatments, can be developed.

http://ocg.cancer.gov/programs/target

http://target.cancer.gov

Cancer Target Discovery and Development (CTD²) Network

The goal of the CTD² Network is to develop and apply new scientific approaches to accelerate the translation of genomic discoveries into novel treatments. To accomplish this, the CTD² Network emphasizes interaction of laboratories with complementary and unique technical expertise in areas such as bioinformatics, genome-wide functional *in vitro* and *ex vivo* screening, protein-protein interactions and small molecule high-throughput screening. These technologies are allowing CTD² to discover functional interactions within the context of specific tumor types.

http://ocg.cancer.gov/programs/ctd2

Cancer Genome Characterization Initiative (CGCI)

CGCI supports research that comprehensively catalogs the alterations in cancer genomes to gain insight into the underlying mechanisms of those cancers. CGCI pushes the limits of cutting-edge genomic sequencing methods to provide the cancer research community high-quality genomic data on selected cancer types such as medulloblastoma, non-Hodgkin lymphoma, and cancers from HIV+ patients.

The HIV+ Tumor Molecular Characterization Project (HTMCP) uses genomic and transcriptomic sequencing to uncover distinct features of diffuse large B-cell lymphomas, lung carcinomas, and cervical carcinomas from HIV+ and HIV- patients.

The Burkitt Lymphoma Genome Sequencing Project (BLGSP) identifies genetic changes in patients with sporadic, endemic, and HIV-associated Burkitt lymphoma to find diagnostic, prognostic, or therapeutic markers or targets for this rare and aggressive cancer.

http://ocg.cancer.gov/programs/cgci

U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES

National Institutes of Health

OFFICE of CANCER GENOMICS

RESOURCES FOR THE RESEARCH COMMUNITY

OCG advances cancer research through collaborative efforts and initiatives that have evolved into successful research programs and valuable resources.

Cancer Genome Anatomy Project (CGAP)

CGAP is a user-friendly online resource for the research and educational community designed to provide access to biological tissue characterization data. CGAP has a wide range of genomic data that includes gene expression profiles of normal, precancerous, and cancerous cells, along with tools for analyzing these data. CGAP also provides a single nucleotide polymorphism analysis of cancer-related genes and the Mitelman database of chromosomal aberrations in cancer.

http://cgap.nci.nih.gov/cgap.html

Cancer Genetic Markers of Susceptibility (CGEMS)

CGEMS is a robust research program that uses collaborative genome-wide association studies (GWAS) to identify common genetic variants that affect individual risk of developing cancer. CGEMS began as a three-year pilot study in 2005 by OCG and NCI's Division of Cancer Epidemiology (DCEG) and is now entirely managed by DCEG. The raw data from CGEMS projects is available for download upon approval.

http://dceg.cancer.gov/research/how-we-study/genomic-studies/cgems-summary/

The ORFeome Collaboration (OC)

The goal of the OC, an informal volunteer multi-institutional collaboration, is to provide the research community a library of human cDNA clones with at least one validated, full open reading frame (ORF) for each of the currently defined human genes. The ORF clones do not include 5′ and 3′ UTRs and can be easily sub-cloned into virtually any type of expression vector.

http://orfeomecollaboration.com/

Mammalian Gene Collection (MGC)

The MGC created an open-access bank of "expression-ready" full-length open reading frame clones for the majority of protein-coding human and mouse genes, as well as some cow and rat genes. Two additional publicly accessible gene collection projects, the Xenopus and Zebrafish Gene Collections, applied the same infrastructure and protocols from MGC.

http://mgc.nci.nih.gov/

DATA SHARING

All data and publications generated by OCG initiatives are shared with the research community through its website. Genomic profiles for a variety of tumor types (including clinical, molecular characterization, and processed sequence data) are easily accessible through a user-friendly Data Matrix specific to each OCG initiative. The program-specific data matrices are maintained by the Data Coordinating Center (DCC) at the NCI Center for Bioinformatics and Information Technology (CBIIT), which manages and stores all data generated for OCG. Through the DCC, the researchers can access up to four levels of data (from raw/trace files through cumulative data) for each chip-based and sequencing platform employed. Raw sequence data is stored at the NCBI Sequence Read Archive (SRA) and accessible through the NCBI database for Genotypes and Phenotypes (dbGaP).
To protect the privacy of the patients, some clinical and genetic data is protected and requires approval to access.

To learn how to gain access to controlled data, visit OCG (*http://ocg.cancer.gov/*) or dbGAP (*http://www.ncbi.nlm.nih.gov/gap*).

OCG e-News

Everyone is invited to check out the **OCG e-News**, an online newsletter featuring research spotlights, educational articles, guest editorials by OCG scientists, and more!

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